THE AMENDMENTS

In the Drawings:

Figure 2, attached herewith, has been amended to label the separate views of the figure as Figure 2A, Figure 2B, Figure 2C and Figure 2D. A clean and marked-up version has been submitted with this Response.

In the Specification:

Please amend the paragraph starting at page 1, line 5 to:

This application is a continuation-in-part of copending application United States Serial No. 09/490,701~~+~~2, filed January 24, 2000, which is incorporated herein in its entirety.

In the Claims:

1. A method for synthesizing a peptide or a peptide-like molecule based on matching a physicochemical mode of a peptide to the same physicochemical mode of a target polypeptide or protein, followed by synthesizing a retro-inverso peptide version of said peptide comprised of D-amino acids, comprising the steps of:

assigning ~~a numerical value of an orderable physicochemical property~~ to each member of a set of peptide constituents a numerical value representative of the hydrophobic free energy of said each member of a set of peptide constituents, said set of peptide constituents including all the members of the set of naturally-occurring L-amino acids;

arranging said peptide constituents in order of said numerical values ~~of said orderable physicochemical property~~;

partitioning said set of peptide constituents into a plurality of peptide constituent groups, whereby each of said peptide constituent groups contains at least one member of said set of peptide constituents, each peptide constituent group encompasses a range of said ordered numerical values, and each member of said set of peptide constituents belongs to only one peptide constitutent group;

creating a polypeptide physicochemical data series by replacing each amino acid in an amino acid sequence of said target polypeptide or protein with said numerical value ~~of said~~